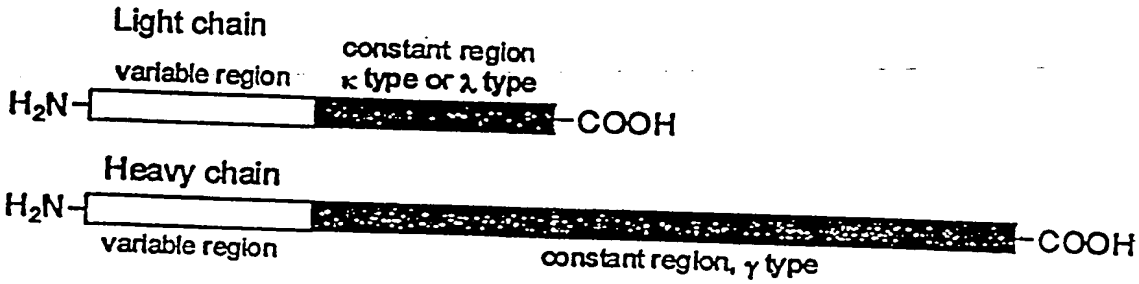

Light chain
variable region
constant region
κ type or λ type
H_2N
COOH
Heavy chain
H_2N
variable region
constant region, γ type
COOH

FIG. 1

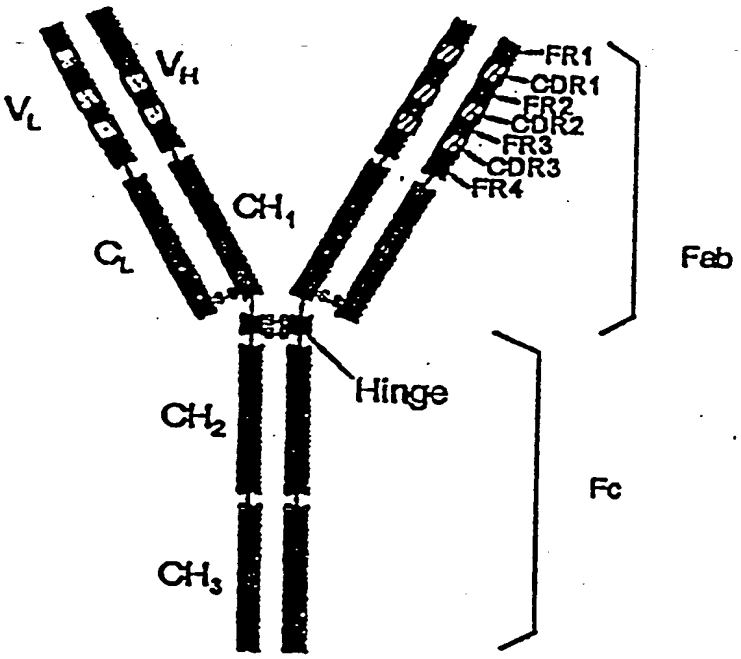


FIG. 2

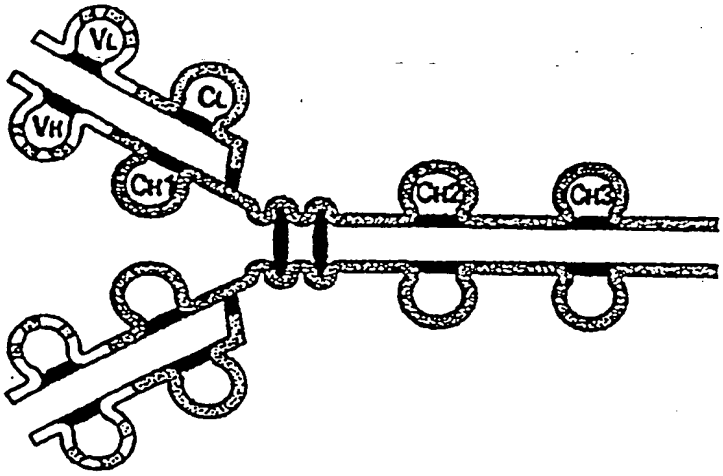


FIG. 3

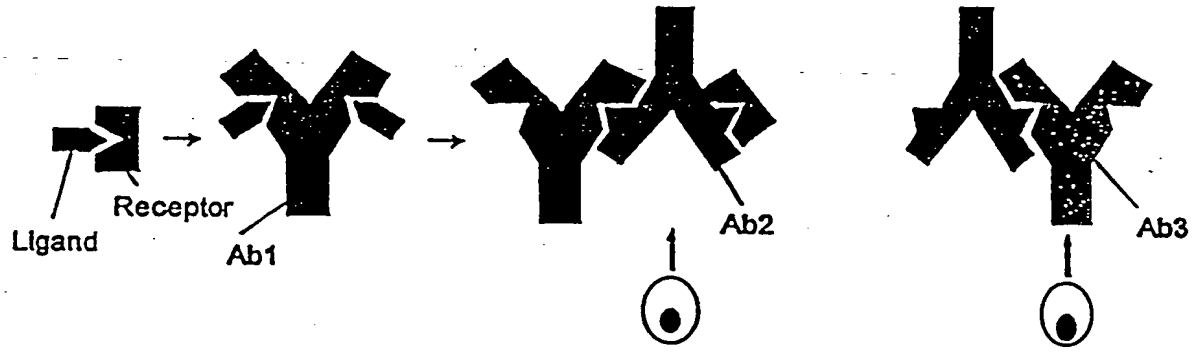


FIG. 4

09831631 09/831631

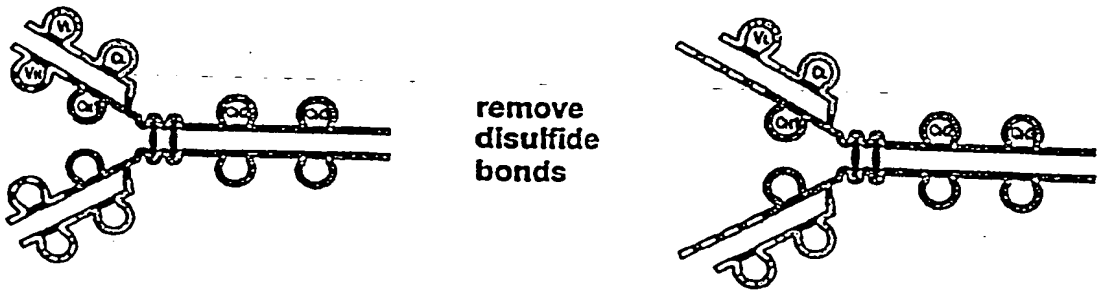


FIG. 5

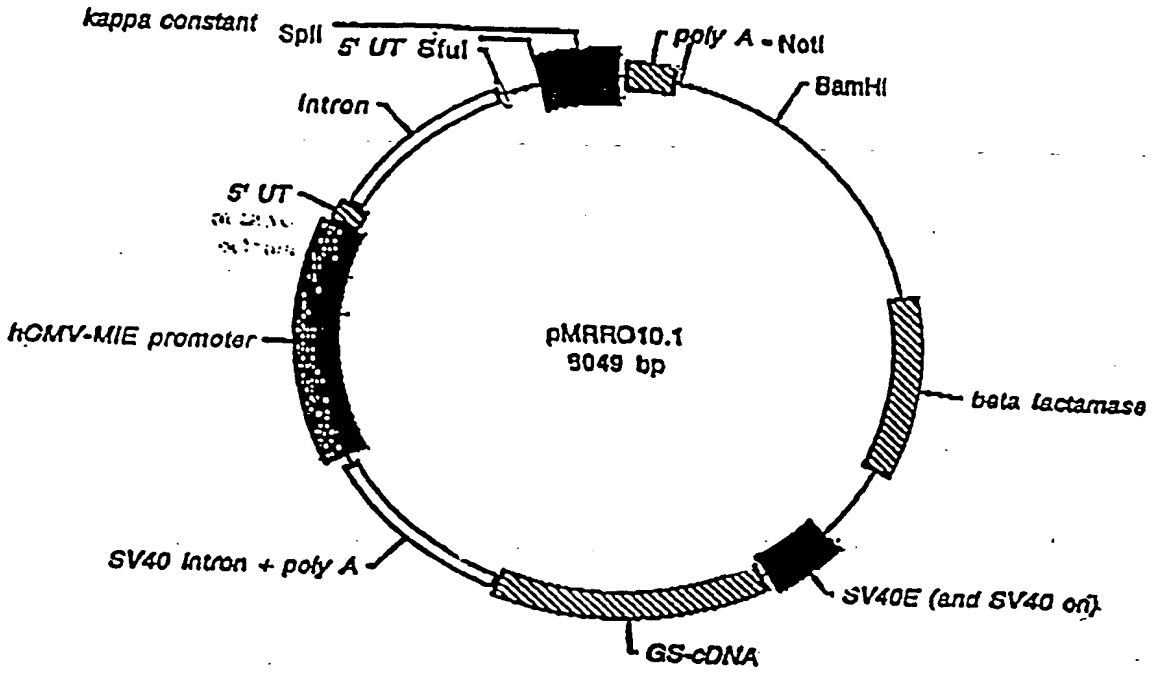

kappa constant
SpII
5' UT
SfuI
poly A - NotI
BamHI
Intron
5' UT
hCMV-MIE promoter
pMRRO10.1
9049 bp
beta lactamase
SV40 Intron + poly A
SV40E (and SV40 ori)
GS-cDNA

FIG. 6A

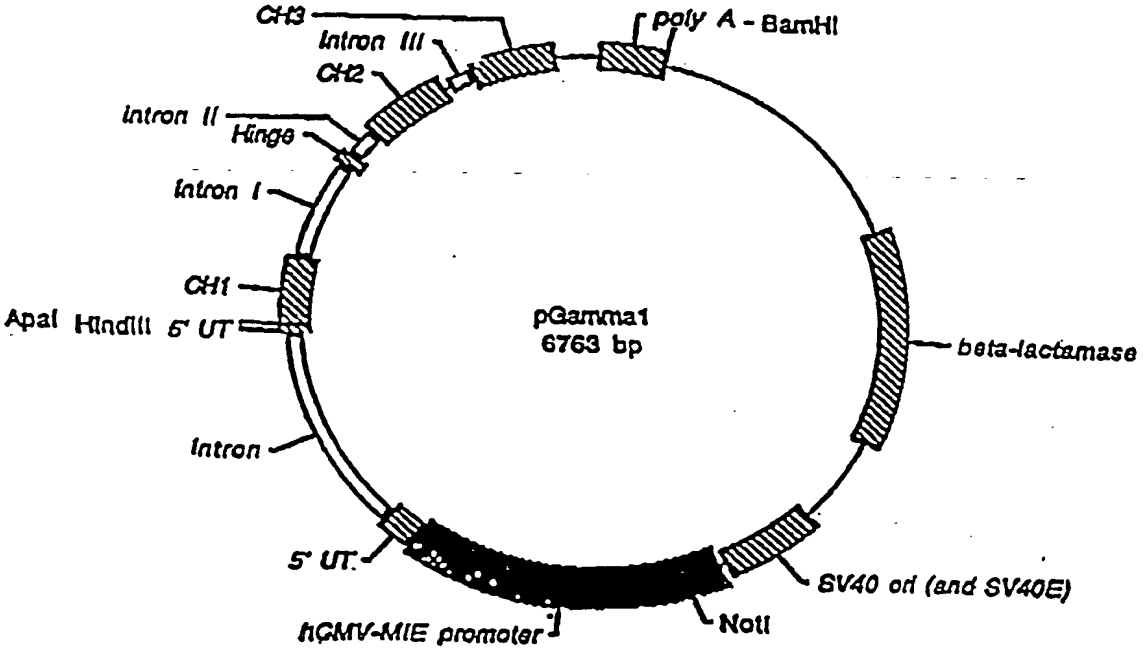

CH3
Intron III
CH2
Intron II
Hinge
Intron I
CH1
ApaI HindIII 5' UT
Intron
5' UT
hCMV-MIE promoter
NotI
SV40 ori (and SV40E)
beta-lactamase
poly A - BamHI
pGamma1
6763 bp

FIG. 6B

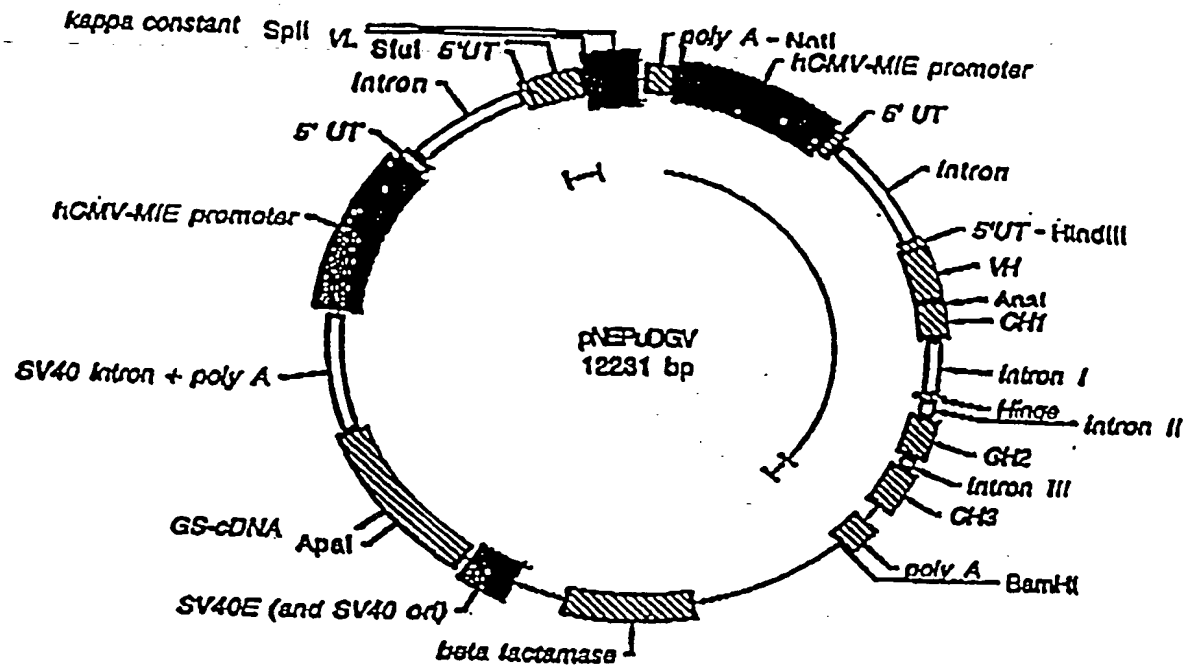

kappa constant
SpII
VL
SfuI
5'UT
Intron
5' UT
hCMV-MIE promoter
SV40 intron + poly A
GS-cDNA
ApaI
SV40E (and SV40 ori)
beta lactamase
poly A - NotI
hCMV-MIE promoter
5' UT
Intron
5'UT - HindIII
VH
AnaI
CH1
Intron I
Hinge
Intron II
CH2
Intron III
CH3
poly A
BamHI
pNEPUDGV
12231 bp

FIG. 6C

ConVL1

EcoR1
GAA TTC

6

-19 (Leader) -1
Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser Ala Gln Ala
ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA
63

V_L:

1 10 20
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr
GAT ATC CAA ATG ACA CAA AGT CCT AGT AGT TTG AGT GCT AGT GTG GGA GAT CGG GTG
ACA 123

21 30 40
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
Pro
ATC ACA TGT CGG GCT AGT CAA AGT ATC AGT AAC TGT TTG GCT TGG TAT CAA CAA AAG
CCT 183

41 50 60
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro
Ser
GGA AAG GCT CCT AAG TTG TTG ATC TAT GCT GCT AGT AGT TTG GAG AGT GGA GTG CCT
AGT 243

61 70 80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Arg Phe Thr Leu Thr Ile Ser Ser Leu Gln
Pro
CGG TTC AGT GGA AGT GGA AGT GGA ACA CGG TTC ACC TTG ACC ATC AGT AGT TTG CAA
CCT 303

81 90 100
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Leu Pro Trp Thr Phe Gly
Gln
GAG GAT TTC GCT ACC TAT TAT TGT CAA CAA TAT AAC AGT TTG CCT TGG ACC TTC GGA
CAA 363

101
Gly Thr Lys Val Glu Ile Lys
GGA ACG AAG GTG GAG ATC AAG GAA TTC 390
EcoRI

FIG. 7A

ConVH1

EcoR1
GAA TTC 6

-19 (Leader) -1
Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala
Gln Ser Ala Gln Ala
ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC
CAA AGT GCC CAA GCA 63

V_L:
1 10 20
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
Gly Ala Ser Val Lys Val
CAG GTT CAG CTG GTG CAG TCT GGC GCT GAG GTG AAG AAG CCT
GGC GCT TCT GTG AAG GTG 123

21 30 35A 35B
40
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Ala Ile
Ser Trp Asn Trp Val Arg Gln Ala
TCT TGC AAG GCT TCT GGC TAC ACA TTC ACA TCT TAC GCT ATA
TCT TGG AAT TGG GTG AGG CAG GCT 189

41 50 60
Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Gly Asn
Gly Asp Thr Asn Tyr Ala
CCT GGC CAG GGC CTG GAG TGG ATG GGC TGG ATA AAT GGA AAT
GGA GAT ACA AAT TAC GCC 249

61 70 80
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
Thr Ser Thr Ala Tyr Met
CAG AAG TTC CAG GGA AGG GTG ACT ATA ACT GCT GAT ACT TCT
ACT TCT ACT GCT TAC ATG 309

81 82A 82B 82C 90
100
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser
GAG CTG TCT TCT CTG AGG TCT GAG GAT ACT GCT GTT TAC TAC
TGC GCT AGG GCT CCT GGC TAC GGC TCT 378

101 110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
GAT TAT TGG GGA CAG GGA ACA CTG GTT ACA GTT TCT TCT GAA TTC
423

FIG. 7B

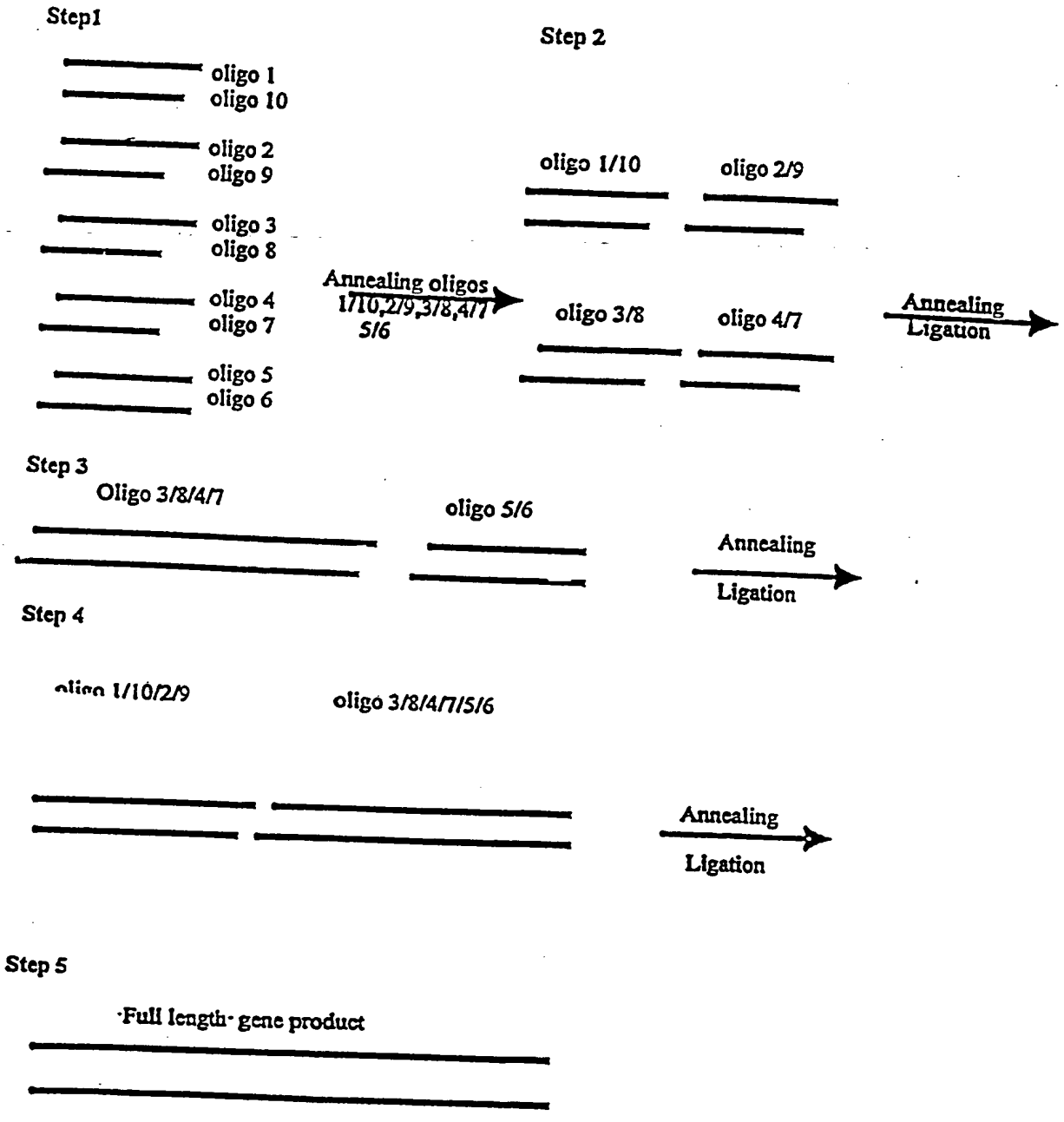

Step1
oligo 1
oligo 10
oligo 2
oligo 9
oligo 3
oligo 8
oligo 4
oligo 7
oligo 5
oligo 6
Annealing oligos 1/10,2/9,3/8,4/7 5/6
Step 2
oligo 1/10
oligo 2/9
oligo 3/8
oligo 4/7
Annealing Ligation
Step 3
Oligo 3/8/4/7
oligo 5/6
Annealing Ligation
Step 4
oligo 1/10/2/9
oligo 3/8/4/7/5/6
Annealing Ligation
Step 5
Full length gene product

FIG. 8

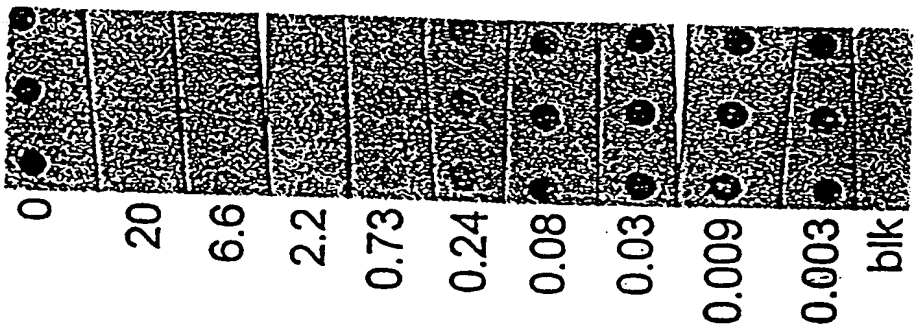
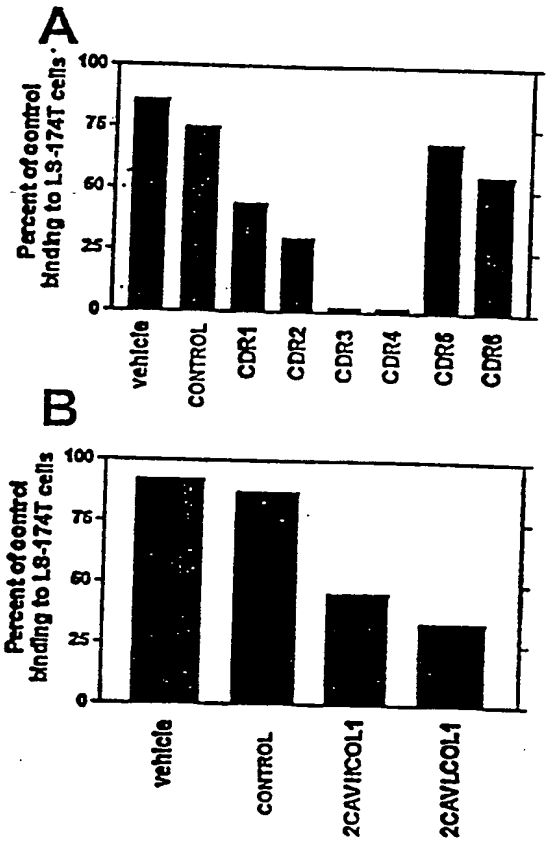
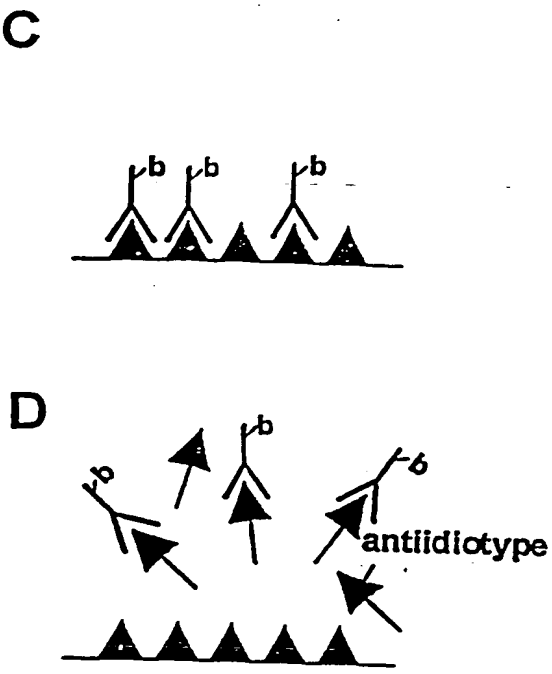


FIG. 9


A
Percent of control binding to L8-174T cells
100
75
50
25
0
vehicle
CONTROL
CDR1
CDR2
CDR3
CDR4
CDR5
CDR6
B
Percent of control binding to L8-174T cells
100
75
50
25
0
vehicle
CONTROL
2CAVHCOL1
2CAVLCOL1


C
b
b
b
D
b
b
b
antiidiotype

FIGS. 10A-D

```
cstacy
DSABL-1  GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACTATG  0.05
      PAGE     83
DSABL-1c
      GCAGCTCATAGTAACCTTCTCTCCAACTGACACAGCTAGGGAGGATGGAGACTGTGACATCACAATGTCTGC
TTGGGC  0.05    PAGE     78
MSAL-CDR1-1   ← GCT in MSALVAC-CDR1-1
      AGCTGCGTCGGCAGCCTCCGAAGCAGCCCGCTCCAGAGCCCGCTGCTCCGATGGTACCAGCAGAAACCAG
GGCAGTCTCCTAAA  0.05    PAGE     84
MSAL-CDR1-1c
      CTGCCCTGGTTTCTGCTGGTACCATCGGAGCAGCGGGCTCTGGAGCGGGCTGCTTCGGAGGCTGCCGAC
      0.05    PAGE     69
```

```
HMVL1   GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACTATGCAGCCCTAAGTCCAGT
HMVL2   CAGAGCCTTTTATATAGTAGCAATCAAAAGATCTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAA
HMVL3   CTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCGGTGGATCTGGG
HMVL5   CCAGCAGCAATATTATAGCATATCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGAATTC
HMVL8   ACGCCTGTGAAGCGATCAGGGATGCCAGATTCCCTAGTGGATGCCCAGTAAATCAGCAGTTTAGGAGA
HMVL9   CTGCCCTGGTTTCTGCTGGTACCAGGCCAAGTACATCTTTTGATTGCTACTATATAAAAGGCTCTGACTGGACTT
HMVL10  AGCGCTCATAGTAACGTTCTCTCCAACTGACACAGCTAGGGAGGATGGAGACTGTGACATCACAATGTCTCCTTGGGC
HMVL6   GAATTCCCGTTTGATTTCCAGCTTGGTGCCTCCACCGAACGTCCGAGGATATCTATAATATTGCTGTGCGTAATAAAC
```

HMVL4

AG AGA TTT GAG TCT CAG CAT CAG GAG TGT GAA GGC TGA AGA CCT GGG
AGT TTA TTA C

HMVL7

TG GGA GGT CTT CAG GCT TCA CAG TGC TGA TGG TGA GAG TGA AAT CTG
TCC CAG ATC C

FIG. 11

A

MSA-63 epitope DNA
GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA CCG CTC GTC
CAG AGC AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC GGC AGC
TGC AGC CGA CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG
CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC

B

MSA-63 protein sequence (Start residue 143 end residue 233)
Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly Glu Gln Val Ser Ser Glu Thr Asn Asp
Lys Glu Asn Asp Ala Met Ser Thr Pro Leu Pro Ser Thr Ser Ala Ala Ile Thr Leu Asn Cys His Thr Cys Ala
Tyr Met Asn Asp Asp Ala Lys Cys Leu Arg Gly Glu Gly Val Cys Thr Thr Gln Asn Ser

C

MSA-63 oligo

MSA1
GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA

MSA2
AGC CCG CTG CTC CGA CCG CTC GTC CAG AGC AGC CTC TGC TTG CTG

MSA3
AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC

MSA4
TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC GAC TTG

MSA5
CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG

MSA6
ATG TAC TTG CTG CTG CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG

MSA7
CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC

FIGS. 12A-C

A

SP-10 Epitope
GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG
GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA GGG GAA CAG GCT TCA GGT
GCA CCA ATT TCA AGC ACA TCT ACA GGC ACA ATA TTA AAT TGC TAC ACA TGT GCT TAT
ATG AAT GAT CAA GGA AAA TGT CTT CGT GGA GAG GGA ACC TGC ATC ACT CAG AAT TC

B

SP-10 protein sequence
Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser gly Glu His Ala
Ser Gly Glu Gln Ala Ser Gly Ala Gln Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala
Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn

C

Oligo SP1:
GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG
GCC TCG GGT GAA CAG CCT TAG

Oligo SP2:
GTG AGC ACG CTT CAG GGG AAC AGG CTT CAG GTG CAC CAA TTT CAA GCA CAT CTA
CAG GCA CAA TAT TAA ATT GCT

Oligo SP3:
ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG AGG GAA CCT
GCA TCA CTC AGA ATT C

Oligo SP3a(3Cys-> Ala):
ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG AGG GAA
CCG CAA TCA CTC AGA ATT C

Oligo SP4:
GAA TTC TGA GTG ATG CAG GTT CCC TCT CCA CGA AGA CAT TTT CCT TGA TCA TTC ATA
TAA GCA CAT GTG TAG CAA TTT A

Oligo SP4a (3Cys->Ala):
GAA TTC TGA GTG ATT GCG GTT CCC TCT CCA CGA AGT GCT TTT CCT TGA TCA TTC ATA
TAA GCT GCT GTG TAG CAA TTT A

Oligo SP5:
ATA TTG TGC CTG TAG ATG TGC TTG AAA TTG GTG CAC CTG AAG CCT GTT CCC CTG AAG
CGT GCT CAC CTG AAG GCT

Oligo SP6:
GTT CTC CCG AGG CCT GCT CAC CAG AAG GCT GTT CAC CGG AGC CAT GTT CAC CTG
AAG GCT GGA ATT C

FIGS. 13A-C

LDH-C_4 Epitope:

Oligo LDH1:
TCG TGC CAG TTC CTC GTC GAC TAG CTC TTC GAC TAG CTC CTG CTG CTC TTG TCG GTC ACG GAA TTC

Oligo LDH2:
GAA TTC CGT GAC CGA CAA GAG CAG CAG GAG CTA GTC GAA GAG CTA GTC GAC GAG GAA CTG GCA CGA CGG GTT CGT

FIG. 14

Leader:

-19 -1
Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser Ala Gln Ala
ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA

Ala GCT V_L in vaccine

1 10 20
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly Glu Lys Val Thr
GAC ATT GTG ATG TCA CAG TCT CCA TCC TCC CTA GCT GTG TCA GTT GGA GAG AAG GTT ACT

21 27 A B C D E F 30 40
Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
ATG AGC TGC AAG TCC AGT CAG AGC CTT TTA TAT AGT AGC AAT CAA AAG ATC TAC TTG GCC TGG TAC CAG CAG AAA CCA

CDR1

41 50 60
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
GGG CAG TCT CCT AAA CTG CTG ATT TAC TGG GCA TCC ACT AGG GAA TCT GGG GTC CCT GAT

CDR2

61 70 80
Arg Phe Thr Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala
CGC TTC ACA GGC GGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT GTG AAG GCT

81 90 100
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gly
GAA GAC CTG GCA GTT TAT TAC TGT CAG CAA TAT TAT AGA TAT CCT CGG ACG TTC GGT GGA

CDR3

101
Gly Thr Lys Leu Glu Ile Lys Arg
GGC ACC AAG CTG GAA ATC AAA CGG

FIG. 15

09583631 09/583,631

2CAVHCOL1

VHC1 5'GAATTCATGGCTTGGGTGTGGACCTTGCTATTCCTGATGGCAGCTGCCCAAAGTGCCC
AAGCACAGATCCAGTTGGTGCA 3'

VHC2 5'GTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCGCTAAGGCTTC
TGGGTATACCTTCACAAACTAG 3'

VHC3 5'GAATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGAT
AAACACCTACACTGGAGAGCCAACA 3'

VHC4 5'TATGCTGATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACT
GCCTATTTGCAGATCAACACCT 3'

VHC5 5'CAAAAATGAGGACACGGCTACATATTTCGCTGCAAGAGCCTACTATGGTAAATAC
TTTGACTACGAATTC 3'

VHC6 5'GAATTCGTAGTCAAAGTATTTACCATAGTAGGCTCTTGCAGCAAATATG 3'

VHC7 5'TAGCCGTGTCCTCATTTTTGAGGTTGTTGATCTGCAAATAGGCAGTGCTGGCAGA
GGTTTCCAAAGAGAAGGCAAACCGT 3'

VHC8 5'CCCTTGAAGTCATCAGCATATGTTGGCTCTCCAGTGTAGGTGTTTATCCAGCCCAT
CCACTTTAAACCCTTTCCTGGAGC 3,

VHC9 5'CTGCTTCACCCAGTTCATTCCATAGTTTGTGAAGGTATACCCAGAAGCCTTAGCGG
AGATCTTGACTGTCTCTCCAGGCT 3'

VHC10 5'TCTTCAGCTCAGGTCCAGACTGCACCAACTGGATCTGTGCTTGGGCACTTTG GGC
AGCTGCCATCAGGAATAGCAAGGTCCACACCCAAGCCATGAATTC 3'

FIG. 16A

2CAVLCOL1

VLC1 5'AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTT
ACCATA 3'

VLC2 5'ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAAACC
AGGGCAG 3'

VLC3 5'TCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCT
TCACTGGCAGT 3'

VLC4 5'GGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCA
GTTTAT 3'

VLC5 5'TTCTGYCAGCAGGATTATAGCTCTCCGCTCACGTTCGGTGCTGGGACCAAGCTGGAG
CTGAAAGAATTC 3'

VLC6 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCACCGAACGTGAGCGGAGAGCTATAATC
CTGCTGACAGAAATAAACTGC 3'

VLC7 5'CAGGTCTTCAGCCTGCACAGTGCTGATGGTGAAAGTGAAATCCGTCCCATATCCA
CTGCCAGT 3'

VLC8 5'GAAGCGATCAGGGACTCCAGTGTAGCGATTGGATGCATAGTATATCAGCAGTTTAG
GAGACTGCCCTGG 3'

VLC9 5'TTTCTGTTGGTACCAAGCTACATCATTACTCACACTCTGACTGGCCTTGCAGGTTA
TGGTAAC 3'

VLC10 5'CCTGTCTCCTGCTGATACAAGCAGGAATTTGGGAGTCTGGGTCATCACAATACTT
GCTTGGGC 3'

VLC11 5'TTCGCTCAGCAGGATTATAGCTCTCCGCTCACGTTCGGTGCTGGGACCAAGCTGG
AGCTGAAAGAATC 3'

VLC12 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCACCGAACGTGAGCGGAGAGCTATAA
TCCTGCTGAGCGAAATAAACTGC 3'

FIG. 16B